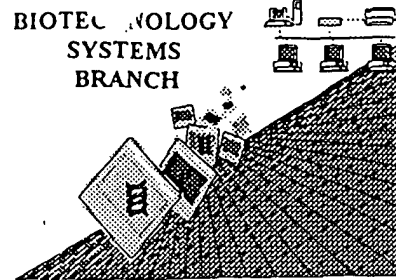


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/785,738

Source: OIPE

Date Processed by STIC: 6-6-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/785,738

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 1 ☐ Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

3 <110> APPLICANT: Sauter, Margret M.
 4 Lorbiecke, Rene
 6 <120> TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
 7 CONDITIONS
 9 <130> FILE REFERENCE: CropDesign
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/785,738
 C--> 12 <141> CURRENT FILING DATE: 2001-02-16
 14 <160> NUMBER OF SEQ ID NOS: 18
 16 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed

pp. 1-11

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 872
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Rice
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (69)..(668)
 27 <400> SEQUENCE: 1
 28 agacgaacaa aaaacagaat ccatacgccat aatcgaaggt tcgctcttgc ttccaccccg 60
 29 caatccac atg gag aac gaa ttc cag gat ggt aag acg gag gtg ata gaa 110
 30 Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu → move to here
 W--> 31 1 5 10
 W--> 33 gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158 Ala Trp
 W--> 34 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His →
 W--> 35 15 20 25 30
 W--> 37 cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206 Arg Glu
 W--> 38 Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly →
 W--> 39 35 40 45
 W--> 41 gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254 Val Ile
 W--> 42 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn →
 W--> 43 50 55 60
 W--> 45 ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302 Leu Lys
 W--> 46 Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys →
 W--> 47 65 70 75
 W--> 49 gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350 Asp Val
 W--> 50 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser →
 W--> 51 80 85 90
 W--> 53 ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt 398 Phe Phe
 W--> 54 Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu →
 W--> 55 95 100 105 110
 W--> 57 gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att 446 Glu Gly
 W--> 58 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile →
 W--> 59 115 120 125
 W--> 61 cgt ata gca ctg aag aaa gga ggc atg att gtt ctg cct gca ggg atg 494 Arg Ile

Format errors.
 Move underlined amino acids to the end of the line.
 Then insert "hard return" where arrows indicate.

RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

W--> 62 Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
 W--> 63 130 135 140
 W--> 65 tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga
 W--> 66 Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
 W--> 67 145 150 155
 W--> 69 ctg ttt gtt ggc gat cct gtt tgg aca ccc tac aac cgt ccc cat gac
 W--> 70 Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
 W--> 71 160 165 170
 W--> 73 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa
 W--> 74 Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
 W--> 75 175 180 185 190
 W--> 77 ggt gaa aat caa gca gtt gaa ggc ttc tga gggttttgtt gggctcctgc
 W--> 78 Asn Gln Ala Val Glu Gly Phe
 W--> 79 195 200
 E--> 81 actgcggttc tatattcaac ctgaataaga tgtgctatag caatgtaaat ttagcacagt 748
 E--> 82 ggctatgggtc gccactcacc aacttgaagt gaaagattta atgatttttg ttaattotta 808
 E--> 83 tgtatcaatc ggcatatagc atttccgaaa tgtgttttca ataaacagga gtcatgaagc 868
 E--> 84 tgaa 872
 121 <210> SEQ ID NO: 3
 122 <211> LENGTH: 980
 123 <212> TYPE: DNA
 124 <213> ORGANISM: Rice
 126 <220> FEATURE:
 127 <221> NAME/KEY: CDS
 128 <222> LOCATION: (139)..(735)
 130 <400> SEQUENCE: 3
 131 cggacgcgtg ggcagattgc gttgagctga agctgttcgt gtgactottc tacaccttcc 60
 132 aggctatccg gaatcgggag ggtttcccaa taggaaagca actcaggact caggagcggc 120
 133 gtctgagagg ttctcagag atg gag aac cag ttc cag gat ggc aag gag gag 171
 134 Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu
 W--> 135 1 5 10
 W--> 137 gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219 Val Ile
 W--> 138 Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
 139 15 20 25
 W--> 141 cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267 Pro His
 W--> 142 His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
 W--> 143 30 35 40
 W--> 145 gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat 315 Glu Leu
 W--> 146 Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
 W--> 147 45 50 55
 W--> 149 gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tot tac atg 363 Asp Glu
 W--> 150 Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
 W--> 151 60 65 70 75
 W--> 153 gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag 411 Asp Ile
 W--> 154 Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
 W--> 155 80 85 90
 W--> 157 ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc 459 Leu Lys
 W--> 158 Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
 W--> 159 95 100 105

Insert
 "hard
 returns"
 where
 arrows
 indicate

Same

RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

W--> 161 tat tgt ctt gag gga agt gga tac ttc gat gtc agg gac caa aat gat 507 Tyr Cys
W--> 162 Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp
W--> 163 110 115 120
W--> 165 cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct 555 Gln Trp
W--> 166 Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro
W--> 167 125 130 135
W--> 169 gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag 603 Ala Gly
W--> 170 Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys
W--> 171 140 145 150 155
W--> 173 gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt 651 Ala Met
W--> 174 Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
W--> 175 160 165 170
W--> 177 ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc 699 Pro His
W--> 178 Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile
W--> 179 175 180 185
W--> 181 aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcataatca 745 Asn Arg
W--> 182 Gly Gly Thr Gln Ala Val Glu Ala Arg
W--> 183 190 195
E--> 185 agatgtgctt cctagtctcg tggtctgtta cactctacag atactgaata aactgtgcta 805
E--> 186 tcagctgttg caatgggctc ctaccgacat cttacatcat ttggcagtat tttgcacaaa 865
E--> 187 cccgcttaaa atctccctga aaatacgcac gtcacatgt cagagtgttt atatacaata 925
E--> 188 atgacacttc agtccacagt cagcaaggga ctaatgacaa aaaaaaaaaa aaaaa 980
225 <210> SEQ ID NO: 5
226 <211> LENGTH: 774
227 <212> TYPE: DNA
228 <213> ORGANISM: Tomato
230 <220> FEATURE:
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (1)..(591)
234 <400> SEQUENCE: 5
W--> 235 gca cca gat cca aga gag gat gtc ata cag gca tgg tac atg gat gac 48 Ala Pro Asp
W--> 236 Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp
W--> 237 1 5 10 15
W--> 239 aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt 96 Asn Asp Glu
W--> 240 Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
W--> 241 20 25 30
W--> 243 gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt 144 Val Ser
W--> 244 Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
W--> 245 35 40 45
W--> 247 gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa 192 Asp Ala
W--> 248 Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
W--> 249 50 55 60
W--> 251 gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa 240 Asp Arg
W--> 252 Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
W--> 253 65 70 75 80
W--> 255 cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg 288 Leu Pro
W--> 256 Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
W--> 257 85 90 95
W--> 259 cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt 336 His Thr

Same

Same

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PATENT APPLICATION: US/09/785,738

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

W--> 260 Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe ↑
 W--> 261 100 105 110
 W--> 263 gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa 384 Asp Val
 W--> 264 Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys ↑
 W--> 265 115 120 125
 W--> 267 ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt 432 Gly Gly
 W--> 268 Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu ↑
 W--> 269 130 135 140
 W--> 271 gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca 480 Asp Ser
 W--> 272 Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro ↑
 W--> 273 145 150 155 160
 W--> 275 att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa 528 Ile Trp
 W--> 276 Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln ↑
 W--> 277 165 170 175
 W--> 279 gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt 576 Glu Tyr
 W--> 280 Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val ↑
 W--> 281 180 185 190
 W--> 283 aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt 631 Asn Ala
 W--> 284 Ala Ala ↑
 W--> 285 195
 E--> 287 aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691
 E--> 288 aatgttgat tgtggcacta aataaatcac ccctatggg agattgattg tttatatgca 751
 E--> 289 agtgaattt attatgtgat ttt 774
 327 <210> SEQ ID NO: 7
 328 <211> LENGTH: 603
 329 <212> TYPE: DNA
 330 <213> ORGANISM: Tomato
 332 <220> FEATURE:
 333 <221> NAME/KEY: CDS
 334 <222> LOCATION: (3)..(572)
 336 <400> SEQUENCE: 7
 W--> 337 aa atg gca atc gag tgt aag gca tgg ttt atg gat gaa aat tca gaa 47 Met Ala
 W--> 338 Ile Glu Cys Lys Ala Trp Phe Met Asp Glu Asn Ser Glu
 W--> 339 1 5 10 15
 W--> 341 gat cag cgg cta ccg cac cag aag aac cca ccg gag ttt gtt tca gtg 95 Asp Gln Arg
 W--> 342 Leu Pro His Gln Lys Asn Pro Pro Glu Phe Val Ser Val
 W--> 343 20 25 30
 W--> 345 gag aaa tta gca gta atc gga gtt tta tac tgg aaa ttg aac cct aat 143 Glu Lys
 W--> 346 Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn
 W--> 347 35 40 45
 W--> 349 gat tac gag aac gat gaa gaa ttg aaa aaa att cgt caa agt aga ggc 191 Asp Tyr
 W--> 350 Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly
 W--> 351 50 55 60
 W--> 353 tac agc tac atg gac ttg ctg gat ttg tgc cct gag aag gtg gat aac 239 Tyr Ser
 W--> 354 Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn
 W--> 355 65 70 75
 W--> 357 tat gag cag aag ttg aaa aat ttc tat acg gag cac ata cac gca gat 287 Tyr Glu
 W--> 358 Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp
 W--> 359 80 85 90 95

Same
error

see

p.1

Same

Error

see

p.1

RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

```

W--> 361 gag gag ata cgt tac tgt ctg gaa ggg agt gga tat ttt gat gtg aga 335 Glu Glu
W--> 362 Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
W--> 363 100 105 110
W--> 365 gac aag gat gat cgc tgg att cgc atc tgg atg aag gcc ggt gat atg 383 Asp Lys
W--> 366 Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met
W--> 367 115 120 125
W--> 369 att gtc ttg cct gct ggg att tac cac cgg ttc acc cta gat act gat 431 Ile Val
W--> 370 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
W--> 371 130 135 140
W--> 372 aac tat gtc aag ttg atg agg ttg ttt gtg gga gag ccg gtg tgg acg 479 Asn Tyr
W--> 373 Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
W--> 374 145 150 155
W--> 376 cct tac aat cga cca caa gaa gat cat cca gca agg aag gag tac atc 527 Pro Tyr
W--> 377 Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile
W--> 378 160 165 170 175
W--> 380 aag agt gtt act gaa aga gta gga gtg cct ctt aca gca cac taa 572 Lys Ser
W--> 381 Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His
W--> 382 180 185 190
E--> 384 gacatatttg agctttacaa acctgagagt g 603
420 <210> SEQ ID NO: 9
421 <211> LENGTH: 889
422 <212> TYPE: DNA
423 <213> ORGANISM: Soybean
425 <220> FEATURE:
426 <221> NAME/KEY: CDS
427 <222> LOCATION: (32)..(634)
429 <400> SEQUENCE: 9
430 cgaacccgtc gtagcagaaa aacttgacac c atg gtt tct tcc gac aag gat 52
431 Met Val Ser Ser Asp Lys Asp
W--> 432 1 5
W--> 434 cca cga gag gat gtc ctt caa gcc tgg tac atg gat gat agt gat gaa 100 Pro Arg
W--> 435 Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
436 10 15 20
W--> 438 gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tcg ttg 148 Asp Gln
W--> 439 Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu
W--> 440 25 30 35
W--> 442 gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat 196 Asp Gln
W--> 443 Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp
W--> 444 40 45 50 55
W--> 446 aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt 244 Asn His
W--> 447 Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
W--> 448 60 65 70
W--> 450 tac acc tac atg gat gtt tgt gag gtc tgc cca gaa aag ttg cca aat 292 Tyr Thr
W--> 451 Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
W--> 452 75 80 85
W--> 454 tat gaa cag aaa atc aaa agc ttc ttt gaa gag cat ctt cac act gat 340 Tyr Glu
W--> 455 Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr Asp
W--> 456 90 95 100
W--> 458 gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg 388 Glu Glu

```

Same

error
see p.1

Same

error
see p.1

RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

```

W--> 459 Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
W--> 460      105                      110                      115
W--> 462 gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg 436 Asp Arg
W--> 463 Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
W--> 464 120                      125                      130                      135
W--> 466 atc atc tta cct gcc gga att tat cat cgc ttt acg cta gat gag agc 484 Ile Ile
W--> 467 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Ser
W--> 468                      140                      145                      150
W--> 470 aac tac att aag gct ttg cgt ttt ttt gtt ggt gag cca gtt tgg act 532 Asn Tyr
W--> 471 Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr
W--> 472                      155                      160                      165
W--> 474 cca tac aat cgt cca aat gac cat ctc cct gca aga caa caa tat gtc 580 Pro Tyr
W--> 475 Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr Val
W--> 476                      170                      175                      180
W--> 478 aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc 628 Lys Asp
W--> 479 Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
W--> 480      185                      190                      195
W--> 482 gcg taa gatctgggttc tgcctaataca tagtaccaca tgaaaaggac caagactttg 684 Ala
W--> 483 200
E--> 485 ttgctaaaagt aaggtttgaa aaaaagaaaa taatggtgtc tttaaataaa gggctcctggc 744
E--> 486 ttgttatgcc ttgatgtacc ctgccagtg tttttgttgc ctgtccctgt ataaagattg 804
E--> 487 cattgtatta ttattagaat tgggtacaga ataaacataa gcataagtta gcatgctgat 864
E--> 488 gtatatattat gtaaaaaaaa ataaa 889
492 <210> SEQ ID NO: 10
493 <211> LENGTH: 200
494 <212> TYPE: PRT
495 <213> ORGANISM: Soybean
497 <400> SEQUENCE: 10
498 Glu Pro Val Val Ala Glu Lys Leu Val Thr Met Val Ser Ser Asp Lys
499 1 5 10 15
500 Asp Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp
501 20 25 30
502 Glu Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser
503 35 40 45
504 Leu Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala
505 50 55 60
506 Asp Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg
507 65 70 75 80
508 Gly Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro
509 85 90 95
510 Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr
511 100 105 110
512 Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val
513 115 120 125
514 Arg Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly
515 130 135 140
516 Met Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
517 145 150 155 160
518 Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp

```

Some

Error

See p. 1

Number of amino acids differ:

- 200 listed

- 210 shown (see next page)

DATE: 05/31/2001

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

```

519                               165                               170                               175
520 Thr Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr
521                               180                               185                               190
522 Val Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala
523                               195                               200                               205
524 Thr Ala
E--> 525 210 → 200 listed
528 <210> SEQ ID NO: 11
529 <211> LENGTH: 933
530 <212> TYPE: DNA
531 <213> ORGANISM: Cotton
533 <220> FEATURE:
534 <221> NAME/KEY: CDS
535 <222> LOCATION: (33)..(635)
537 <400> SEQUENCE: 11
538 attttttttt aatttgacgg aaaaaaaaaa ct atg acc atg ggt tct gca gac 53
539 Met Thr Met Gly Ser Ala Asp
W--> 540                                1                                5
W--> 542 aag agg gag gaa gtt att cag gca tgg tac atg gat gat agt gat gaa 101 Lys Arg
W--> 543 Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
544                10                        15                        20
W--> 546 gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg 149 Asp Gln
W--> 547 Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu
W--> 548        25                        30                        35
W--> 550 gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat 197 Asp Lys
W--> 551 Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp
W--> 552 40                        45                        50                        55
W--> 554 aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt 245 Asn Tyr
W--> 555 Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
W--> 556                60                        65                        70
W--> 558 tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat 293 Tyr Ser
W--> 559 Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
W--> 560                75                        80                        85
W--> 562 tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat 341 Tyr Glu
W--> 563 Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp
W--> 564                90                        95                        100
W--> 566 gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg 389 Glu Glu
W--> 567 Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg
W--> 568        105                        110                        115
W--> 570 gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg 437 Asp His
W--> 571 Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
W--> 572 120                        125                        130                        135
W--> 574 ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac 485 Ile Val
W--> 575 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
W--> 576                140                        145                        150
W--> 578 aac tat att aag gca atg cgg ctc ttt gtt ggt gat cca att tgg act 533 Asn Tyr
W--> 579 Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr
W--> 580                155                        160                        165
W--> 582 ccg tac aat cgt ccg cac gat cat ctt cct gca agg aag gag tat atc 581 Pro Tyr

```

Some
Format
error

> refer
to
p.i

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

```

W--> 583 Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
W--> 584          170          175          180
W--> 586 aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc 629 Lys Asn
W--> 587 Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
W--> 588          185          190          195
W--> 590 gca taa aatcaacatt catctggtgg tggccaagtc gttgatgctg cgcataaaaa 685 Ala
W--> 591 200
E--> 593 tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgtggttaata 745
E--> 594 aataagtcta ggcttgctcg cttttgatgc gtggatatgg atcgttatgg ttgttgcttg 805
E--> 595 ctatatattg cctattccat atcgaaaatt cgcaaacctg ctatgtatctt ctacatttta 865
E--> 596 tgtgcttact accagattgg ctcttaataa tcaaagttta cataatatac atttcgtcga 925
E--> 597 cgcggccg 933
633 <210> SEQ ID NO: 13
634 <211> LENGTH: 919
635 <212> TYPE: DNA
636 <213> ORGANISM: Human
638 <220> FEATURE:
639 <221> NAME/KEY: CDS
640 <222> LOCATION: (1)..(564)
642 <400> SEQUENCE: 13

W--> 643 cga aca cgg cac ccg cac tgc gcg tca gtg gtg cag gcc tgg tat atg 48 Arg Thr Arg
W--> 644 His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
W--> 645 1 5 10 15
W--> 647 gac gac gcc ccg ggc acc cgc ggc aac ccc acc gcc ccg acc ccg gcc 96 Asp Asp Ala
W--> 648 Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
W--> 649 20 25 30
W--> 651 gcc cag tgc gct gga gca gct gcg cgg ctc ggg gtg ctc tac tgg aag 144 Ala Gln
W--> 652 Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
W--> 653 35 40 45
W--> 655 ctg gat gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga 192 Leu Asp
W--> 656 Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
W--> 657 50 55 60
W--> 659 aga gag agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat 240 Arg Glu
W--> 660 Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
W--> 661 65 70 75 80
W--> 663 aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat 288 Lys Leu
W--> 664 Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
W--> 665 85 90 95
W--> 667 ttg cac ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac 336 Leu His
W--> 668 Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
W--> 669 100 105 110
W--> 671 ttc gat gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag 384 Phe Asp
W--> 672 Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
W--> 673 115 120 125
W--> 675 aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg 432 Lys Gly
W--> 676 Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
W--> 677 130 135 140
W--> 679 gtg gac gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa 480 Val Asp
W--> 680 Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu

```

Same
see p.1Same
see
p.1

RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

```

W--> 681 145          150          155          160
W--> 683 ccg gtg tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc 528 Pro Val
W--> 684 Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
W--> 685          165          170          175
W--> 687 ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgtctgcc 574 Gly Gln
W--> 688 Tyr Val Lys Phe Leu Ala Gln Thr Ala
W--> 689          180          185
E--> 691 tgggaactaa cacgtgcctc gtaaagggtcc ccaatgtaat gaactgagca gaaaattcaa 634
E--> 692 tcaacttttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga 694
E--> 693 ttatttgatc agaataattt gtaatgaaag gatctagaaa gcaacttgga agtgtaaaga 754
E--> 694 gtcacotttca ttttctgtaa ctcaatcaag actggtgggt ccatggccct gtgtagttc 814
E--> 695 attgcattca gggtgagtc caaatgaaag tttcatctcc cgaaatgcag ttccttagat 874
E--> 696 gcccatctgg acgtgaatgc cgcgcctgcg tgtaagaagg tgcaat 920
732 <210> SEQ ID NO: 15
733 <211> LENGTH: 972
734 <212> TYPE: DNA
735 <213> ORGANISM: Mouse
737 <220> FEATURE:
738 <221> NAME/KEY: CDS
739 <222> LOCATION: (17)..(556)
741 <400> SEQUENCE: 15
742 agccgcgcc gccacc atg gtg cag gcc tgg tat atg gac gag tcc acc gcc 52
743 Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala
W--> 744          1          5          10
W--> 746 gac ccg cgg aag ccc cac cgc gca cag ccc gac cgc ccc gtg agc ctg 100 Asp Pro
W--> 747 Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
748          15          20          25
W--> 750 gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac 148 Glu Gln
W--> 751 Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
W--> 752          30          35          40
W--> 754 aag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac 196 Lys Tyr
W--> 755 Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
W--> 756 45          50          55          60
W--> 758 tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat 244 Tyr Ser
W--> 759 Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn
W--> 760          65          70          75
W--> 762 tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat 292 Tyr Glu
W--> 763 Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp
W--> 764          80          85          90
W--> 766 gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg 340 Glu Glu
W--> 767 Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
W--> 768          95          100          105
W--> 770 gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg 388 Asp Lys
W--> 771 Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met
W--> 772          110          115          120
W--> 774 att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag 436 Ile Thr
W--> 775 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys
W--> 776 125          130          135          140
W--> 778 aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca 484 Asn Tyr

```

Same
See P.1

Same
See P.1

RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

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Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

W--> 779 Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
W--> 780 145 150 155
W--> 782 cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg 532 Pro Tyr
W--> 783 Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met
W--> 784 160 165 170
W--> 786 agt ttt ttg gaa gga aca gca tag cagtgtcct caaagagaaa actgcactgt 586 Ser Phe
W--> 787 Leu Glu Gly Thr Ala
W--> 788 175 180
E--> 790 gtgaatctcc tgctgtggtg accgaatgga aagttgtctca cttttctgct tttgtatttg 646
E--> 791 aacttgaggc tagactagct ctctttgcta ggattgtgag atcagtgtct tttaaataaa 706
E--> 792 agcctctcta aaagtgaagt ttacatggaa gccacaaaaa tgtgaaaaag tgacctaat 766
E--> 793 tttccctaac tgtcaagact tagaggtata ggagccctgg attggtatgt gcattcatgc 826
E--> 794 atggccaatc ttcattctccc agatcttttag gtgtctgttg gtgtgaagct atgcctcctg 886
E--> 795 caagagggca gttataacca gcacaactaa ccagatgacg tttttctcct ttgctgattg 946
E--> 796 ttgagtgggg aagtgggggtt gttgtt 972

799 <210> SEQ ID NO: 16

800 <211> LENGTH: 179

801 <212> TYPE: PRT

802 <213> ORGANISM: Mouse

804 <400> SEQUENCE: 16

805 Ala Ala Ala Ala Thr Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr

806 1 5 10 15

807 Ala Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser

808 20 25 30

809 Leu Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala

810 35 40 45

811 Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg

812 50 55 60

813 Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro

814 65 70 75 80

815 Asn Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu

816 85 90 95

817 Asp Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val

818 100 105 110

819 Arg Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp

820 115 120 125

821 Met Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu

822 130 135 140

823 Lys Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp

824 145 150 155 160

825 Thr Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr

826 165 170 175

827 Met Ser Phe Leu Glu Gly Thr Ala

3--> 828 180

831 <210> SEQ ID NO: 17

832 <211> LENGTH: 706

833 <212> TYPE: DNA

834 <213> ORGANISM: Zebrafish

836 <220> FEATURE:

Same
see
p. 1

Number of aminos differ:
- 179 listed
- 184 shown

RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

837 <221> NAME/KEY: CDS

838 <222> LOCATION: (36)..(581)

840 <400> SEQUENCE: 17

841 gtactgcgca tggagaccga accggactgt tcaag atg agt gtt ttc gag gca 53

842 Met Ser Val Phe Glu Ala

W--> 843
 W--> 845 tgg tac atg gat gaa gag tcc gga gag gac cag aga ctc ccg cac aaa 101 Trp Tyr
 W--> 846 Met Asp Glu Glu Ser Gly Glu Asp Gln Arg Leu Pro His Lys
 847 10 15 20
 W--> 849 ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga 149 Leu Ser
 W--> 850 Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly
 W--> 851 25 30 35
 W--> 853 gtc ttt cac tgg aag ctg aac gct gat atc tat gaa aat gac ccc gaa 197 Val Phe
 W--> 854 His Trp Lys Leu Asn Ala Asp Ile Tyr Glu Asn Asp Pro Glu
 W--> 855 40 45 50
 W--> 857 ctg cag aag atc cga gag gag aag ggt tat tcc ttt atg gac atc ata 245 Leu Gln
 W--> 858 Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile
 W--> 859 55 60 65 70
 W--> 861 acc att cac ccg gac aaa ctg ccc gat tac caa aac aaa ctg aaa atg 293 Thr Ile
 W--> 862 His Pro Asp Lys Leu Pro Asp Tyr Gln Asn Lys Leu Lys Met
 W--> 863 75 80 85
 W--> 865 ttt tac gaa gag cat ctc cac ctg gac gat gag atc cgt tat att ctg 341 Phe Tyr
 W--> 866 Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu
 W--> 867 90 95 100
 W--> 869 gaa gga tcc tct tat ttt gat gtg cgg gac gaa ggc gac cgc tgg atc 389 Glu Gly
 W--> 870 Ser Ser Tyr Phe Asp Val Arg Asp Glu Gly Asp Arg Trp Ile
 W--> 871 105 110 115
 W--> 873 cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att 437 Arg Ile
 W--> 874 Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
 W--> 875 120 125 130
 W--> 877 tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt 485 Tyr His
 W--> 878 Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg
 W--> 879 135 140 145 150
 W--> 881 ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat 533 Leu Phe
 W--> 882 Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
 W--> 883 155 160 165
 W--> 885 gac ttt gac atc cgc aag gaa tac gtg aac tgc ctg gga agc tcc tga 581 Asp Phe
 W--> 886 Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
 W--> 887 170 175 180
 W--> 889 atgcctgat gggattgatt tagtgctgag aatcagactc tgcggtgcct taaacagaca 641
 W--> 890 tgcagcaata gtagagctaa catgtcatta cttagtcac aagacacacc tgatataaag 701
 W--> 891 attat 706

Missing mandatory <220> to <223>
 features to explain the "n's" in

the sequence

See #9 on the

Error
Summary
Sheet.

Same
error.
see p.1

VERIFICATION SUMMARY

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

TIME: 10:36:55

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:33 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:37 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:73 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:77 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81 M:254 E: No. of Bases conflict, LENGTH:Input:748 Counted:170 SEQ:1
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:808 Counted:230 SEQ:1
L:83 M:254 E: No. of Bases conflict, LENGTH:Input:868 Counted:290 SEQ:1
L:84 M:254 E: No. of Bases conflict, LENGTH:Input:872 Counted:294 SEQ:1
L:84 M:252 E: No. of Seq. differs, <211>LENGTH:Input:872 Found:294 SEQ:1
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:137 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:141 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17

VERIFICATION SUMMARY

DATE: 05/31/2001

PATENT APPLICATION: US/09/785,738

TIME: 10:36:55

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:145 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:149 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:153 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:157 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:161 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:165 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:169 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:173 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:177 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:181 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:185 M:254 E: No. of Bases conflict, LENGTH:Input:805 Counted:231 SEQ:3
L:186 M:254 E: No. of Bases conflict, LENGTH:Input:865 Counted:291 SEQ:3
L:187 M:254 E: No. of Bases conflict, LENGTH:Input:925 Counted:351 SEQ:3
L:188 M:254 E: No. of Bases conflict, LENGTH:Input:980 Counted:406 SEQ:3
L:188 M:252 E: No. of Seq. differs, <211>LENGTH:Input:980 Found:406 SEQ:3
L:235 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:236 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:239 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:240 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:243 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:247 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:248 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

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L:251 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:252 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:255 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:259 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:260 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:263 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:267 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:271 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:275 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:279 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:283 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:287 M:254 E: No. of Bases conflict, LENGTH:Input:691 Counted:60 SEQ:5
L:288 M:254 E: No. of Bases conflict, LENGTH:Input:751 Counted:120 SEQ:5
L:289 M:254 E: No. of Bases conflict, LENGTH:Input:774 Counted:143 SEQ:5
L:289 M:252 E: No. of Seq. differs, <211>LENGTH:Input:774 Found:143 SEQ:5
L:337 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:341 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:342 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:345 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:349 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:350 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:353 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:357 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7

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L:361 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:362 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:365 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:369 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:372 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:374 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:376 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:377 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:380 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:381 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:384 M:254 E: No. of Bases conflict, LENGTH:Input:603 Counted:31 SEQ:7
L:384 M:252 E: No. of Seq. differs, <211>LENGTH:Input:603 Found:31 SEQ:7
L:432 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:434 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:434 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:435 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:438 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:438 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:439 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:442 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:442 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:443 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:446 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:446 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:447 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:448 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:450 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:450 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:451 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:452 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:454 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:454 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:455 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9

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L:456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:458 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:458 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:459 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:460 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:462 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:462 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:463 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:466 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:466 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:467 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:470 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:470 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:471 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:472 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:474 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:474 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:475 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:475 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:478 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:478 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:479 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:482 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:482 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:485 M:254 E: No. of Bases conflict, LENGTH:Input:744 Counted:112 SEQ:9
L:486 M:254 E: No. of Bases conflict, LENGTH:Input:804 Counted:172 SEQ:9
L:487 M:254 E: No. of Bases conflict, LENGTH:Input:864 Counted:232 SEQ:9
L:488 M:254 E: No. of Bases conflict, LENGTH:Input:889 Counted:257 SEQ:9
L:488 M:252 E: No. of Seq. differs, <211>LENGTH:Input:889 Found:257 SEQ:9
J:525 M:252 E: No. of Seq. differs, <211>LENGTH:Input:200 Found:210 SEQ:10
J:540 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
J:542 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
J:542 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
J:543 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
J:543 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
J:546 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
J:546 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
J:547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
J:547 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11

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L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:550 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:550 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:551 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:552 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:554 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:554 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:555 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:555 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:558 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:558 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:559 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:559 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:562 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:562 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:563 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:563 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:566 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:566 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:567 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:567 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:568 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:570 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:570 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:571 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:571 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:574 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:574 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:575 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:575 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:576 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:578 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:578 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:579 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:579 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:582 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:582 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:583 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:583 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:584 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:586 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:586 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:587 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11

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L:587 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:588 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:590 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:590 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:591 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:593 M:254 E: No. of Bases conflict, LENGTH:Input:745 Counted:113 SEQ:11
L:594 M:254 E: No. of Bases conflict, LENGTH:Input:805 Counted:173 SEQ:11
L:595 M:254 E: No. of Bases conflict, LENGTH:Input:865 Counted:233 SEQ:11
L:596 M:254 E: No. of Bases conflict, LENGTH:Input:925 Counted:293 SEQ:11
L:597 M:254 E: No. of Bases conflict, LENGTH:Input:933 Counted:301 SEQ:11
L:597 M:252 E: No. of Seq. differs, <211>LENGTH:Input:933 Found:301 SEQ:11
L:643 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:644 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:645 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:647 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:648 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:649 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:651 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:652 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:655 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:656 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:657 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:659 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:660 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:663 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:664 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:667 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:668 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:669 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:671 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:672 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:675 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:676 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:677 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:679 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:680 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:681 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:683 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:684 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:687 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:688 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:691 M:254 E: No. of Bases conflict, LENGTH:Input:634 Counted:60 SEQ:13
L:692 M:254 E: No. of Bases conflict, LENGTH:Input:694 Counted:120 SEQ:13

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L:693 M:254 E: No. of Bases conflict, LENGTH:Input:754 Counted:180 SEQ:13
L:694 M:254 E: No. of Bases conflict, LENGTH:Input:814 Counted:240 SEQ:13
L:695 M:254 E: No. of Bases conflict, LENGTH:Input:874 Counted:300 SEQ:13
L:696 M:254 E: No. of Bases conflict, LENGTH:Input:920 Counted:346 SEQ:13
L:696 M:252 E: No. of Seq. differs, <211>LENGTH:Input:919 Found:346 SEQ:13
L:744 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:746 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:750 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:752 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:754 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:756 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:758 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:759 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:760 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:762 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:764 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:766 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:767 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:768 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:770 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:772 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:774 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:776 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:778 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:780 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:782 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:784 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:786 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12
L:787 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:790 M:254 E: No. of Bases conflict, LENGTH:Input:646 Counted:112 SEQ:15
L:791 M:254 E: No. of Bases conflict, LENGTH:Input:706 Counted:172 SEQ:15
L:792 M:254 E: No. of Bases conflict, LENGTH:Input:766 Counted:232 SEQ:15
L:793 M:254 E: No. of Bases conflict, LENGTH:Input:826 Counted:292 SEQ:15
L:794 M:254 E: No. of Bases conflict, LENGTH:Input:886 Counted:352 SEQ:15
L:795 M:254 E: No. of Bases conflict, LENGTH:Input:946 Counted:412 SEQ:15
L:796 M:254 E: No. of Bases conflict, LENGTH:Input:972 Counted:438 SEQ:15
L:796 M:252 E: No. of Seq. differs, <211>LENGTH:Input:972 Found:438 SEQ:15
L:828 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:828 M:252 E: No. of Seq. differs, <211>LENGTH:Input:179 Found:184 SEQ:16
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001

TIME: 10:36:55

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

L:845 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:846 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:849 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:850 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:853 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:854 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:857 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:858 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:859 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:861 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:862 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:865 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:866 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:869 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:870 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:873 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:874 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:877 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:881 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:885 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:889 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:889 M:254 E: No. of Bases conflict, LENGTH:Input:641 Counted:113 SEQ:17
L:890 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:890 M:254 E: No. of Bases conflict, LENGTH:Input:701 Counted:173 SEQ:17
L:891 M:254 E: No. of Bases conflict, LENGTH:Input:706 Counted:178 SEQ:17
L:891 M:252 E: No. of Seq. differs, <211>LENGTH:Input:706 Found:178 SEQ:17